THE UNIVERSITY of EDINBURGH

Edinburgh Research Explorer

Mapping QTL for performance and carcass traits in chicken chromosomes 6, 7, 8, 11 and 13

Citation for published version:
Moura, ASAMT, Boschiero, C, Campos, RLR, Ambo, M, Nones, K, Ledur, MC, Rosario, MF, Melo, CMR, Burt, D & Coutinho, LL 2006, 'Mapping QTL for performance and carcass traits in chicken chromosomes 6, 7, 8, 11 and 13', Paper presented at 8th World Congress on Genetics Applied to Livestock Production, Belo Horizonte, Brazil, 13/08/06 - 18/08/06.

Link:
Link to publication record in Edinburgh Research Explorer

Document Version:
Peer reviewed version

General rights
Copyright for the publications made accessible via the Edinburgh Research Explorer is retained by the author(s) and / or other copyright owners and it is a condition of accessing these publications that users recognise and abide by the legal requirements associated with these rights.

Take down policy
The University of Edinburgh has made every reasonable effort to ensure that Edinburgh Research Explorer content complies with UK legislation. If you believe that the public display of this file breaches copyright please contact openaccess@ed.ac.uk providing details, and we will remove access to the work immediately and investigate your claim.

OPEN ACCESS

Download date: 07. May. 2023

MAPPING QTL FOR PERFORMANCE AND CARCASS TRAITS IN CHICKEN CHROMOSOMES 6, 7, 8, 11 AND 13

A.S.A.M.T. Moura[1], C. Boschiero[1], R. L.R. Campos[2], M. Ambo[2], K.Nones[2,6], M.C. Ledur[3], M.F. Rosario[2], C.M.R. Melo[4], D.W. Burt[5], L.L. Coutinho[2]

[1] UNESP FMVZ, Botucatu, SP, 18618-000, Brazil; [2] USP ESALQ, Av. Pádua Dias, 11, Piracicaba, SP, 13418-900, Brazil; [3] Embrapa Suínos e Aves, BR 153, Km 110, Concórdia, SC, 89700-000, Brazil; [4] UFSC, Rodovia Edmar Gonzaga, 1346, Florianópolis, SC, 88040-900, Brazil; [5] Roslin Institute (Edinburgh), Midlothian EH25 9PS, UK; [6] Present address: AgResearch Limited – Grasslands, Private Bag 1008 Palmerston North, New Zealand

INTRODUCTION

Our group has developed a chicken F2 resource population for QTL mapping. In previous studies we identified QTL affecting body weight, feed intake, carcass traits and organs weights on four regions of chromosome 1 (Nones *et al*., 2006), and also on chromosomes 2 to 5 (Baron, 2004 and Ruy, 2004). In this report, we focused on chromosomes 6, 7, 8, 11 and 13. QTL for body weight at 6 and 9 weeks of age, fatness, meat yield, and muscle distribution were previously identified on chromosomes 6, 7, 8, 11, and 13 by Ikeobi *et al.* (2002), Sewalen *et al.* (2002), Ikeobi *et al.* (2004) and Jennen *et al.* (2004). Thus, the objective of this study was to map QTL for performance, carcass traits and organs weight on chicken chromosomes 6 to 8, 11, and 13 in the Brazilian F2 resource population.

MATERIAL AND METHODS

Experimental population and data recording. An F2 chicken population specially designed for QTL mapping studies was originated from the crossbreeding of seven males from a broiler line and seven females from a layer line at *Embrapa Suínos e Aves*, Concórdia, Brazil. From a total of 2,063 F2 chickens incubated over a period of 8 months, 356 belonging to four full-sib families were used in this study. F2 chickens were reared as broilers up to 42 d of age. They were individually caged from 35 to 41 d, when feed intake was recorded allowing the computation of feed conversion. Body weight was recorded at 1, 35, 41, and 42 d. At the latter age, recording was performed after 6 h fasting and transportation to the slaughterhouse. Carcasses were eviscerated, stored at – 4^{o}C for six hours and dissected. Weights of heart, lungs, gizzard, liver and feet, as well as the length of intestine were recorded before chilling. Weights of carcass, breast, drums and thighs, wings, residual carcass and abdominal fat were recorded after chilling. Blood samples were collected at slaughter for further DNA analysis.

Genotyping. 26 microsatellite markers covering 100% of the consensus maps of chromosomes 7, 8, and 11, 71.6% of chromosome 13, and 47.3% of chromosome 6 were used to genotype 10 parental, 6 F1, and up to 356 F2 chickens (Table 1). Individual PCR reactions using fluorescent primers were conducted for each marker. PCR products from three to four markers were mixed for allele size determinations in a *MegaBACE* genotyper (*GE Healthcare*). Linkage maps were constructed for the five chromosomes using multipoint linkage analyses (Ambo *et al*., 2005; Boschiero *et al*., 2005; Campos *et al*., 2005).

Table 1. Number of markers, map length and first marker used in the QTL analyses

Chromosome	Number of markers	Map length (cM)	First marker	F2 genotyped
6	4	33.7	*ROS0062*	73 to 355
7	8	116.9	*LEI0064*	172 to 355
8	5	82.6	*ABR0322*	342 to 356
11	4	105.5	*LEI0143*	304 to 317
13	5	57.0	*ADL0147*	301 to 313

QTL mapping analyses. Phenotypic data were submitted to a preliminary analysis of variance including effects of hatch, sex, family and their two-way interactions. Adjustments for hatch and significant interactions were then performed and the residuals used in the QTL interval mapping analyses using the regression method (Haley *et al.,* 1994) and the line cross genetic model of the *QTL Express* software (Seaton, 2002). Sex and family effects were included in the model for QTL mapping only if significant. Body weight at 35 d was used as a covariate for weight gain and feed intake from 35 to 41 d, whereas body weight at 42 d was used for carcass weight, carcass traits and organs weight. Significance thresholds were computed using a permutation test (Churchill and Doerge, 1994) and probability levels for significant (5%) and suggestive genomewise linkage were used (Lander and Kruglyak, 1995).

RESULTS AND DISCUSSION

A suggestive QTL affecting five growth-related traits and also feed intake was mapped between markers *ADL0315* and *ADL0169* on chromosome 7 (Table 2). QTL for body weight at 3, 6 and 9 wk of age were previously identified on this chromosome by Sewalen et al. (2002), but in a different and four times as long interval: *LEI0064 – ROS0019* (101 cM according to the consensus map). Suggestive QTL associated with feet weight were detected on chromosomes 6 and 11, with gizzard weight on chromosomes 8 and 11, and with heart weight on chromosome 13 (Table 2).

All QTL, except for that affecting gizzard weight on chromosome 8, showed positive additive effects (Table 3), indicating that the allele that confers higher weights and feed intake originated from the broiler line. The QTL affecting gizzard weight on chromosome 8 showed negative additive effect, suggesting that the allele for high gizzard weight, in this particular case, originated from the layer line (Table 3). The two QTL for feet weight on chromosomes 6 and 11 showed significant dominance effects, but with opposite signs (Table 3).

The test statistic of the QTL for heart weight on chromosome 13 (F = 8.37) was very close to the 5% genomewise threshold (F = 8.70). Additionally, this QTL explained 4.34% of the phenotypic variance of heart weight (Table 3), indicating that it may be of interest to the poultry industry, considering that cardio-respiratory capacity is related to metabolic problems such as sudden death and ascites in broilers.

Table 2. QTL that exceeded suggestive linkage

Chromosome	Trait (g)	Position (cM)[A]	Flanking markers	F
6	Feet weight	4	*ROS0062 – ROS0003*	6.02
7	Body weight at 35 d	116	*ADL0315 – ADL0169*	6.40
	Body weight at 42 d	116	*ADL0315 – ADL0169*	6.55
	Weight gain from birth to 35 d	116	*ADL0315 – ADL0169*	6.28
	Weight gain from birth to 42 d	116	*ADL0315 – ADL0169*	6.46
	Feed intake from 35 to 41 d	116	*ADL0315 – ADL0169*	6.30
8	Gizzard weight	62	*ABR0345 – ADL0172*	6.55
11	Gizzard weight	43	*ADL0123 – ADL0210*	5.94
	Feet weight	46	*ADL0123 – ADL0210*	5.74
13	Heart weight	39	*MCW0110 – MCW0104*	8.37

[A] Position from the first marker in the chromosome set

Table 3. Additive and dominance effects (standard errors) and the proportion of the phenotypic variance explained by the QTL

Chromosome	Trait (g)	Additive effect	Dominance effect	Phenotypic variance (%)
6	Feet weight	0.85 (0.36)	1.60 (0.71)	2.80
7	Body weight at 35 d	40.81 (11.60)	26.10 (25.84)	2.99
	Body weight at 42 d	53.74 (15.10)	34.52 (33.64)	3.07
	Weight gain from birth to 35 d	40.49 (11.62)	26.10 (25.87)	2.93
	Weight gain from birth to 42 d	53.42 (15.12)	34.52 (33.67)	3.03
	Feed intake from 35 to 41 d	30.94 (8.85)	19.11 (18.51)	2.95
8	Gizzard weight	-1.20 (0.33)	-0.08 (0.63)	3.08
11	Gizzard weight	1.10 (0.35)	-1.25 (0.65)	2.98
	Feet weight	1.13 (0.39)	-1.67 (0.73)	2.87
13	Heart weight	0.43 (0.10)	0.13 (0.15)	4.34

CONCLUSION AND FUTURE WORK

The QTL mapped for weight gain and feed intake on chromosome 6, and the one for heart weight on chromosome 13 should be subjected to further investigation. Despite the fact that the linkage evidence was mild (suggestive linkage), they point out to candidate regions for genes affecting traits of great economic relevance to the poultry industry.

For the chromosomes involved in this study, genotyping is being extended to one more full-sib family, with approximately 100 F2 chickens to improve the power to detect QTL (Alfonso and Haley, 1998). Another ongoing effort is to genotype markers for the remaining chromosomes (9, 10, 12, 14 to 24 and Z) in these five full-sib families in order to complete the genome scan for performance and carcass traits.

ACKNOWLEDGEMENTS

Financial support was provided by EMBRAPA/PRODETAB and by FAPESP (Fundação de Amparo à Pesquisa do Estado de São Paulo), which also granted scholarships to C. Boschiero, R.L. Campos, M. Ambo, K. Nones and M.F. Rosario. A.S.A.M.T. Moura, C.M.R. Melo and L.L. Coutinho were sponsored by CNPq.

REFERENCES

Alfonso, L. and Haley, C.S. (1998) *Anim. Sci*. **66**:1-8.

Ambo, M., Moura, A.S.A.M.T., Campos, R.L.R., Nones, K., Rosario, M.F., Boschiero, C., Ledur, M., Coutinho, L.L. (2005) *Proc. 51st Brazilian Genetics Congress*. 166.

Baron, E.E. (2004) PhD Thesis, University of São Paulo. Piracicaba, Brazil.

Boschiero, C., Rosario, M.F., Campos, R.L.R, Ambo, M., Coutinho, L.L., Ledur, M., Moura, A.S.A.M.T. (2005) *Proc. 51st Brazilian Genetics Congress*. 38.

Campos, R.L.R., Ambo, M., Moura, A.S.A.M.T., Nones, K., Rosario, M.F., Boschiero, C., Ledur, M., Coutinho, L.L. (2005) *Proc. 51st Brazilian Genetics Congress*. 121.

Churchill G.A. and Doerge R.W. (1994) *Genetics* **138**: 963-971.

Haley C.S., Knott S.A., Elsen J.M. (1994) *Genetics* **136**: 1195-1207**.**

Ikeobi, C.O.N., Woolliams, J.A., Morrice, D.R., Law, A., Windsor, D., Burt, D.W., Hocking, P.M. (2002) *Anim. Genet.* **33**: 428-435.

Ikeobi, C.O.N., Woolliams, J.A., Morrice, D.R., Law, A., Windsor, D., Burt, D.W., Hocking, P.M. (2004) *Livest. Prod. Sci.* **87**: 143-151.

Jennen, D.G.J., Vereijken, A.L.J., Bovenhuis, H., Crooijmans, R.P.M.A., Veenendaal, A., Van Der Poel, J. J., Groenen, M.A.M. (2004) *Poult. Sci.* **83**: 295-301.

Lander, E. and Kruglyak, L. (1995) *Nature Genetics*, **11**: 241-247.

Nones, K., Ledur, M.C., Ruy, D.C., Baron, E.E., Melo, C.M.R., Moura, A.S.A.M.T., Zanella, E.L., Burt, D.W., Coutinho, L.L. (2006) *Anim. Genet.* (in press).

Ruy, D.C. (2004) PhD Thesis, University of São Paulo. Piracicaba, Brazil.

Seaton G., Haley C.S., Knott S.A., Kearsey M., Visscher P.M. (2002) *Bioinformatics* **18**: 339-340.

Sewalen, A., Morrice, D.R., Law, A., Windsor, Haley, C.S., Ikeobi, C.O.N., Burt, D.W., Hocking, P.M. (2002) *Poult. Sci.* **81**: 1775-1781.